

SEQUENCE LISTING

- T470X
- (1) GENERAL INFORMATION:
- (i) APPLICANT: Lyman, Stewart D.
Beckmann, M. Patricia
 - (ii) TITLE OF INVENTION: Ligands for flt3 Receptors
 - (iii) NUMBER OF SEQUENCES: 8
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: Washington
 - (E) COUNTRY: US
 - (F) ZIP: 98101
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Macintosh 7.0.1
 - (D) SOFTWARE: Microsoft Word, Version #5.1
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: -to be assigned-
 - (B) FILING DATE: March 7, 1994
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/162,407
 - (B) FILING DATE: December 3, 1993
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/111,758
 - (B) FILING DATE: August 25, 1993
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/106,463
 - (B) FILING DATE: August 12, 1993
 - (C) CLASSIFICATION:
 - (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/068,394
 - (B) FILING DATE: May 24, 1993
 - (C) CLASSIFICATION:
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Malaska, Stephen L.
 - (B) REGISTRATION NUMBER: 32,655
 - (C) REFERENCE/DOCKET NUMBER: 2813-D
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 587-0430
 - (B) TELEFAX: (206) 233-0644
 - (C) TELEX: 756822
- 47

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..25

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 855..879

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 57..752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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GTCGACTGGA ACGAGACGAC CTGCTCTGTC ACAGGCATGA GGGGTCCCCG GCAGAG      56

ATG ACA GTG CTG GCG CCA GCC TGG AGC CCA AAT TCC TCC CTG TTG CTG      104
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu
  1              5              10              15

CTG TTG CTG CTG CTG AGT CCT TGC CTG CGG GGG ACA CCT GAC TGT TAC      152
Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr
              20              25              30

TTC AGC CAC AGT CCC ATC TCC TCC AAC TTC AAA GTG AAG TTT AGA GAG      200
Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu
              35              40              45

TTG ACT GAC CAC CTG CTT AAA GAT TAC CCA GTC ACT GTG GCC GTC AAT      248
Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn
              50              55              60

CTT CAG GAC GAG AAG CAC TGC AAG GCC TTG TGG AGC CTC TTC CTA GCC      296
Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala
  65              70              75              80

CAG CGC TGG ATA GAG CAA CTG AAG ACT GTG GCA GGG TCT AAG ATG CAA      344
Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln
              85              90              95

ACG CTT CTG GAG GAC GTC AAC ACC GAG ATA CAT TTT GTC ACC TCA TGT      392
Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys
              100              105              110

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IMMUNEX CORPORATION

2813-E

| | | | | | | | | | | | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|---------|-----|-------|-------|-------|-------|-----|-----|-----|-----|
| ACC | TTC | CAG | CCC | CTA | CCA | GAA | TGT | CTG | CGA | TTC | GTC | CAG | ACC | AAC | ATC | 440 |
| Thr | Phe | Gln | Pro | Leu | Pro | Glu | Cys | Leu | Arg | Phe | Val | Gln | Thr | Asn | Ile | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| TCC | CAC | CTC | CTG | AAG | GAC | ACC | TGC | ACA | CAG | CTG | CTT | GCT | CTG | AAG | CCC | 488 |
| Ser | His | Leu | Leu | Lys | Asp | Thr | Cys | Thr | Gln | Leu | Leu | Ala | Leu | Lys | Pro | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| TGT | ATC | GGG | AAG | GCC | TGC | CAG | AAT | TTC | TCT | CGG | TGC | CTG | GAG | GTG | CAG | 536 |
| Cys | Ile | Gly | Lys | Ala | Cys | Gln | Asn | Phe | Ser | Arg | Cys | Leu | Glu | Val | Gln | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| TGC | CAG | CCG | GAC | TCC | TCC | ACC | CTG | CTG | CCC | CCA | AGG | AGT | CCC | ATA | GCC | 584 |
| Cys | Gln | Pro | Asp | Ser | Ser | Thr | Leu | Leu | Pro | Pro | Arg | Ser | Pro | Ile | Ala | |
| | | | | 165 | | | | | 170 | | | | | | 175 | |
| CTA | GAA | GCC | ACG | GAG | CTC | CCA | GAG | CCT | CGG | CCC | AGG | CAG | CTG | TTG | CTC | 632 |
| Leu | Glu | Ala | Thr | Glu | Leu | Pro | Glu | Pro | Arg | Pro | Arg | Gln | Leu | Leu | Leu | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| CTG | CTG | CTG | CTG | CTG | CCT | CTC | ACA | CTG | GTG | CTG | CTG | GCA | GCC | GCC | TGG | 680 |
| Leu | Leu | Leu | Leu | Leu | Pro | Leu | Thr | Leu | Val | Leu | Leu | Ala | Ala | Ala | Trp | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| GGC | CTT | CGC | TGG | CAA | AGG | GCA | AGA | AGG | AGG | GGG | GAG | CTC | CAC | CCT | GGG | 728 |
| Gly | Leu | Arg | Trp | Gln | Arg | Ala | Arg | Arg | Arg | Gly | Glu | Leu | His | Pro | Gly | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| GTG | CCC | CTC | CCC | TCC | CAT | CCC | TAGGATT | CGA | GCCTT | GTGCA | TCGTT | GACTC | | | | 779 |
| Val | Pro | Leu | Pro | Ser | His | Pro | | | | | | | | | | |
| 225 | | | | | 230 | | | | | | | | | | | |
| AGCCAGGGTC | TTATCTCGGT | TACACCTGTA | ATCTCAGCCC | TTGGGAGCCC | AGAGCAGGAT | | | | | | | | | | | 839 |
| TGCTGAATGG | TCTGGAGCAG | GTCGTCTCGT | TCCAGTCGAC | | | | | | | | | | | | | 879 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Thr | Val | Leu | Ala | Pro | Ala | Trp | Ser | Pro | Asn | Ser | Ser | Leu | Leu | Leu | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Leu | Leu | Leu | Leu | Leu | Ser | Pro | Cys | Leu | Arg | Gly | Thr | Pro | Asp | Cys | Tyr | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Phe | Ser | His | Ser | Pro | Ile | Ser | Ser | Asn | Phe | Lys | Val | Lys | Phe | Arg | Glu | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Leu | Thr | Asp | His | Leu | Leu | Lys | Asp | Tyr | Pro | Val | Thr | Val | Ala | Val | Asn | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |

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Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala
 65 70 75 80
 Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln
 85 90 95
 Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys
 100 105 110
 Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile
 115 120 125
 Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
 130 135 140
 Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
 145 150 155 160
 Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
 165 170 175
 Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
 180 185 190
 Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp
 195 200 205
 Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly
 210 215 220
 Val Pro Leu Pro Ser His Pro
 225 230

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACTGGAA CGAGACGACC TGCT

24

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGCAGGTCGT CTCGTTCCAG

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 988 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 30..734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | | | | | | | | | | | | | |
|------------|------------|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CGGCCGGAAT | TCCGGGGCCC | CCGGCCGAA | ATG | ACA | GTG | CTG | GCG | CCA | GCC | TGG | | 53 | | | | |
| | | | Met | Thr | Val | Leu | Ala | Pro | Ala | Trp | | | | | | |
| | | | 1 | | | | 5 | | | | | | | | | |
| AGC | CCA | ACA | ACC | TAT | CTC | CTC | CTG | CTG | CTG | CTG | AGC | TCG | GGA | CTC | 101 | |
| Ser | Pro | Thr | Thr | Tyr | Leu | Leu | Leu | Leu | Leu | Leu | Ser | Ser | Gly | Leu | | |
| | 10 | | | | | 15 | | | | 20 | | | | | | |
| AGT | GGG | ACC | CAG | GAC | TGC | TCC | TTC | CAA | CAC | AGC | CCC | ATC | TCC | TCC | GAC | 149 |
| Ser | Gly | Thr | Gln | Asp | Cys | Ser | Phe | Gln | His | Ser | Pro | Ile | Ser | Ser | Asp | |
| | 25 | | | | 30 | | | | | 35 | | | | | 40 | |
| TTC | GCT | GTC | AAA | ATC | CGT | GAG | CTG | TCT | GAC | TAC | CTG | CTT | CAA | GAT | TAC | 197 |
| Phe | Ala | Val | Lys | Ile | Arg | Glu | Leu | Ser | Asp | Tyr | Leu | Leu | Gln | Asp | Tyr | |
| | | | | 45 | | | | | 50 | | | | | 55 | | |
| CCA | GTC | ACC | GTG | GCC | TCC | AAC | CTG | CAG | GAC | GAG | GAG | CTC | TGC | GGG | GGC | 245 |
| Pro | Val | Thr | Val | Ala | Ser | Asn | Leu | Gln | Asp | Glu | Glu | Leu | Cys | Gly | Gly | |
| | | | 60 | | | | | 65 | | | | | 70 | | | |
| CTC | TGG | CGG | CTG | GTC | CTG | GCA | CAG | CGC | TGG | ATG | GAG | CGG | CTC | AAG | ACT | 293 |
| Leu | Trp | Arg | Leu | Val | Leu | Ala | Gln | Arg | Trp | Met | Glu | Arg | Leu | Lys | Thr | |
| | | 75 | | | | | 80 | | | | | 85 | | | | |
| GTC | GCT | GGG | TCC | AAG | ATG | CAA | GGC | TTG | CTG | GAG | CGC | GTG | AAC | ACG | GAG | 341 |
| Val | Ala | Gly | Ser | Lys | Met | Gln | Gly | Leu | Leu | Glu | Arg | Val | Asn | Thr | Glu | |
| | 90 | | | | | 95 | | | | | 100 | | | | | |
| ATA | CAC | TTT | GTC | ACC | AAA | TGT | GCC | TTT | CAG | CCC | CCC | CCC | AGC | TGT | CTT | 389 |
| Ile | His | Phe | Val | Thr | Lys | Cys | Ala | Phe | Gln | Pro | Pro | Pro | Ser | Cys | Leu | |
| 105 | | | | | 110 | | | | | 115 | | | | | 120 | |

CGC TTC GTC CAG ACC AAC ATC TCC CGC CTC CTG CAG GAG ACC TCC GAG 437
 Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu
 125 130 135

CAG CTG GTG GCG CTG AAG CCC TGG ATC ACT CGC CAG AAC TTC TCC CGG 485
 Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg
 140 145 150

TGC CTG GAG CTG CAG TGT CAG CCC GAC TCC TCA ACC CTG CCA CCC CCA 533
 Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro
 155 160 165

5 TGG AGT CCC CGG CCC CTG GAG GCC ACA GCC CCG ACA GCC CCG CAG CCC 581
 Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro
 170 175 180

CCT CTG CTC CTC CTA CTG CTG CTG CCC GTG GGC CTC CTG CTG CTG GCC 629
 Pro Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala
 185 190 195 200

GCT GCC TGG TGC CTG CAC TGG CAG AGG ACG CGG CGG AGG ACA CCC CGC 677
 Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg
 205 210 215

CCT GGG GAG CAG GTG CCC CCC GTC CCC AGT CCC CAG GAC CTG CTG CTT 725
 Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu
 220 225 230

GTG GAG CAC TGACCTGGCC AAGGCCTCAT CCTGCGGAGC CTAAACAAC 774
 Val Glu His
 235

GCAGTGAGAC AGACATCTAT CATCCCATTT TACAGGGGAG GATACTGAGG CACACAGAGG 834

GGAGTCACCA GCCAGAGGAT GTATAGCCTG GACACAGAGG AAGTTGGCTA GAGGCCGGTC 894

CCTTCCTTGG GCCCCTCTCA TTCCCTCCCC AGAATGGAGG CAACGCCAGA ATCCAGCACC 954

GGCCCCATTT ACCCAACTCT GAACAAAGCC CCCG 988

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu
 1 5 10 15

Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe
 20 25 30

Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu
 35 40 45
 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu
 50 55 60
 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln
 65 70 75 80
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly
 85 90 95
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala
 100 105 110
 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser
 115 120 125
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp
 130 135 140
 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro
 145 150 155 160
 Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
 165 170 175
 Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu Leu Leu Leu Leu Leu Leu
 180 185 190
 Pro Val Gly Leu Leu Leu Leu Ala Ala Ala Trp Cys Leu His Trp Gln
 195 200 205
 Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly Glu Gln Val Pro Pro Val
 210 215 220
 Pro Ser Pro Gln Asp Leu Leu Leu Val Glu His
 225 230 235

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATTGGTACC TTTGGATAAA AGAGACTACA AGGACGACGA TGACAAGACA CCTGACTGTT 60
 ACTTCAGCCA C 71

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG

37